A Specific Mutation in the Promoter Region of the Silent cel Cluster Accounts for the Appearance of Lactose-Utilizing Lactococcus lactis MG1363

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SUPPLEMENTAL MATERIAL

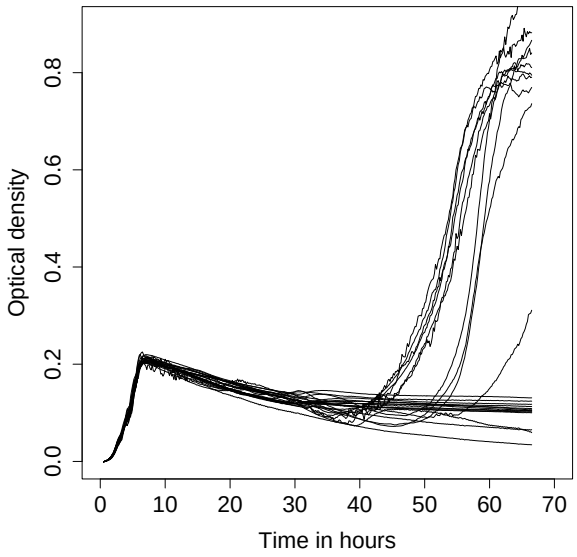
Strain or plasmid	Description	Source or reference
E. coli DH5α	F- ϕ80*lacZ*Δ*M15* Δ(*lacZYA-argF) U169 rec1A end1A hsd*R17 *gyrA96 supE4 4thi-1 relA1*	Invitrogen (Carlsbad, CA)
L. lactis strains		
MG1363 (=MGwt)	*L. lactis* subsp. *cremoris* plasmid-free derivative of NCDO712 (Prt^-, Lac^-).	2
NZ9000	Derivative of MG1363 carrying *pepN::nisRK*	3
HB21 (=MGLac^+)	Lac^+ derivative of MG1363, carrying an A to G transition at nt 174861 in the genome sequence at NCBI (Acc. Nr.: NC_009004)	This work
MGLac^+*nisRK*	MGLac^+ carrying *pseudo10*::*nisRK*	This work
MGLac^+*nisRK*Δ*celB*	MGLac^+*nisRK* carrying a chromosomal deletion of *celB*	This work
MGLac^+Δ*ptcBA*	MGLac^+ carrying a chromosomal deletion of *ptcBA*	This work
MGLac^+Δ*bglS*	MGLac^+ carrying a chromosomal deletion of *bglS*	This work
MGLac^+P*cel-gfp*	MGLac^+ carrying a single chromosomal copy of pSEUDO::P*cel-gfp*	This work
MGLac^+P*cel*-gfp*	MGLac^+ carrying a single chromosomal copy of pSEUDO::P*cel*-gfp*	This work
MGLac^+Δ*ccpA*P*cel*-gfp*	MGLac^+ carrying a chromosomal deletion of *ccpA*.	
MGLac^+*nisRK* Δ*celB* pNZ*celB*	Derivative of MGLac^+*nisRK* with deletion of *celB* carrying pNZ*celB*	This work
Plasmids		

pSEUDO-GFP	Em^r, with GFP-SF, for integration in *L. lactis* pseudogene 10	5
pJWV102_gfp	Amp^r, Tet^r, with *gfp** behind P*czcD*	Veening, manuscript in preparation
pSEUDO-gfp*	Em^r, derivative of pSEUDO-GFP carrying *gfp** for integration in *L. lactis* pseudogene 10	This work
pCS1966::*pseudo10*::*nisRK*	Em^r, with *nisRK* genes, for integration in *L. lactis* pseudogene 10	5
pNZ8048	Cm^r, gene expression vector carrying a nisin-inducible P*nisA*	1
pNZ*celB*	pNZ8048 *celB* behind P*nisA*	This work
pILORI4	Em^r; pIL252 carrying the multiple cloning site and promoterless *lacZ* of pORI13	4
pILORI4::P*cel*	pILORI4, *lacZ* behind P*cel*	This work
pILORI4::P*cel**	pILORI4, *lacZ* behind P*cel**	This work
pCS1966	Em^r, *L. lactis* integration vector, OroP-based selection	6
pCS1966-*celB*'	pCS1966 containing *celB* deletion construct	This work
pCS1966-*ptcBA*'	pCS1966 containing *ptcBA* deletion construct	This work
pCS1966-*bglS*'	pCS1966 containing *bglS* deletion construct	This work
pCS1966-*ccpA'*	pCS1966 containing *ccpA* deletion construct	This work
pSEUDO::P*cel*-gfp	pSEUDO-gfp* with P*cel*	This work
pSEUDO::P*cel**-gfp	pSEUDO-gfp* with P*cel**	This work

S1. Strains and plasmids used in this study.

Primer	Sequence (5'to 3')	Enzyme
KocelB1F	GCATTCTAGACAGACGGTGTTCGACTTGAC	*XbaI*
KocelB2R	GCATGGATCCCGCAGTAATTCCGTTCATGG	*BamHI*
KocelB3F	GCATGGATCCCGCAGCTAACAAGTTGGAAG	*BamHI*
KocelB4R	CGTACTCGAGGATTCCCAGCCGCCATACAG	*XhoI*
KoPtcBA1F	GCATTCTAGATCGGGATTTGGCAAGTCAGG	*XbaI*
KoPtcBA2R	GCATGGATCCGCACATGCAAGTGCAATAAC	*BamHI*
KoPtcBA3F	GCATGGATCCCAAGAACGACGCCTTCAAGC	*BamHI*
KoPtcBA4R	CGTACTCGAGGGTAATTGCCTCGTTAAGTC	*XhoI*
Pllmg_0186ZR	GCATTCTAGATCCGCCTCAAAGTTTGAACG	*XbaI*
Pllmg_0186F	CCGCTAGCATGCAAGCCATACTTCGTGAATAC	*SphI*
CelB_F	AGATCCATGGATGAACGGAATTACTGCGTGGATGGAG	*NcoI*
CelB_Rev	GATCTCTAGATAAATCTTACCAGATTTAAC	*XbaI*
KobglS1F	GCATTCTAGATCGTTATCTGGGTACCATTC	*XbaI*
KobglS2Rev	GCATGGATCCTTCCATATTATTCCCCCACTGG	*BamHI*
KobglS3F	GCATGGATCCAAACAAAGAGCACTCAAGTG	*BamHI*
KobglS4Rev	CGTACTCGAGCTTTGAAAGCCTCCGTTCAC	*XhoI*
CelB_F	AGATCCATGGATGAACGGAATTACTGCGTGGATGGAG	*NcoI*
CelB_R	GATCTCTAGATAAATCTTACCAGATTTAAC	*XbaI*
0186_1Rev	TCCACCATCACTTCCATTCC	-
0186_2Rev	TGATTGGCATAATTTACAAC	-
0186_3Rev	AAAGCTGCAAGTACTCCTTC	-
0186_4Rev	GCAAGTACTCCTTCTTTATC	-
gfp_sf_F	GCATCTCGAGTACTGATTAACTAATAAGGAGGACAAAC	*XhoI*
gfp_sf_R	CGATGGATCCGAAATACGGGCAGACATGGC	*BamHI*

S2. Primers used in this study.



S3. Growth of 24 individual cultures of MG1363(Lac$^-$) in M17 medium supplemented with lactose. All the cultures eventually started to grow on lactose.

Gene name	Locus	Bayesian p	Fold	Function
llmg_0186	*llmg_0186*	2.68E-10	85.6	outer suface protein, β-glucosidase motif
galP	*llmg_2237*	2.61E-10	40.9	galactose permease, the Leloir pathway
llmg_0188	*llmg_0188*	6.96E-06	38.5	protein of unknown function
celB	*llmg_0187*	6.53E-06	37.1	PTS system, cellobiose-specific IIC component
hadL	*llmg_0254*	4.88E-09	26.5	cryptic haloacid dehalogenase
galM	*llmg_2236*	2.94E-10	24.7	galactose mutarotase, the Leloir pathway
metC	*llmg_1776*	1.34E-09	24.6	cystathionine gamma-synthase
galK	*llmg_2235*	5.69E-10	22.0	galactokinase, the Leloir pathway
tnp905	*llmg_2493*	7.17E-10	17.4	transposase for insertion sequence element IS905N
oppF	*llmg_0698*	5.03E-09	16.0	oligopeptide transport ATP-ase
cysK	*llmg_1775*	1.28E-08	14.3	O-acetylserine sulfhydrylase
llmg_2164	*llmg_2164*	1.44E-09	14.0	protein of unknown function, CesSR regulon
cspA	*llmg_1847*	4.97E-09	11.9	cold shock-like protein CspA
tnp905	*llmg_2493*	1.35E-08	10.7	transposase for insertion sequence element IS905N
llmg_1330	*llmg_1330*	4.87E-09	9.7	putative membrane protein
llmg_0334	*llmg_0334*	2.89E-07	8.8	putative thiamine transporter
oppA	*llmg_0701*	2.71E-08	8.7	oligopeptide transport ATP-ase
oppB	*llmg_0699*	4.62E-06	8.3	oligopeptide transport ATP-ase
adhE	*llmg_2432*	6.94E-08	8.3	bifunctional acetaldehyde-CoA/alcohol dehydrogenase
plpB	*llmg_0336*	2.48E-08	8.2	D-methionine-binding lipoprotein precursor
thiE	*llmg_1218*	1.08E-07	7.9	thiamine-phosphate pyrophosphorylase
galT	*llmg_2234*	1.09E-08	7.9	galactose 1-P uridylyltransferase, the Leloir pathway
oppC	*llmg_0700*	3.72E-07	7.7	oligopeptide transport ATP-ase
oppD	*llmg_0697*	1.12E-07	7.5	oligopeptide transport ATP-ase

pfl	*llmg_0629*	1.57E-08	7.4	pyruvate formate lyase
llmg_0301	*llmg_0301*	3.52E-08	7.2	MerR family transcriptional regulator
ps431	*llmg_2111*	8.05E-07	7.1	pseudogene (prophage gene)
galE	*llmg_2233*	2.27E-07	7.1	UDP-galactose-4-epimerase, the Leloir pathway
argG	*llmg_0138*	8.52E-08	7.1	arginine metabolism
llmg_2163	*llmg_2163*	1.01E-07	7.0	protein of unknown function, CesSR regulon
argH	*llmg_0139*	3.01E-08	7.0	arginine metabolism
llmg_pseudo02	*llmg_pseudo02*	7.05E-08	6.9	pseudogene 02 (MFS transporter)
llmg_0281	*llmg_0281*	2.09E-08	6.3	anaerobic ribonucleoside triphosphate reductase
murB	*llmg_1329*	7.19E-08	6.2	UDP-N-acetylenolpyruvoylglucosamine reductase
busAB	*llmg_1049*	5.31E-08	6.1	glycine betaine/proline ABC transporter
noxE	*llmg_0408*	1.38E-08	6.0	NADH oxidase
vacB1	*llmg_1586*	1.94E-08	6.0	exoribonuclease
pyrB	*llmg_0893*	2.87E-08	5.5	pyrimidine metabolism
vacB1	*llmg_1586*	5.99E-08	5.3	exoribonuclease
llmg_0099	*llmg_0099*	3.85E-08	5.1	50S ribosomal protein L32
cspD2	*llmg_1238*	4.11E-05	5.0	cold shock-like protein
llmg_2194	*llmg_2194*	9.30E-08	4.9	protein of unknown function
llmg_0070	*llmg_0070*	8.25E-08	4.8	putative permease
pyrC	*llmg_1508*	1.95E-06	4.6	pyrimidine metabolism
llmg_2322	*llmg_2322*	1.86E-07	4.6	protein of unknown function
nusG	*llmg_2388*	2.69E-06	4.6	transcription antitermination protein
carA	*llmg_0894*	5.15E-07	4.5	carbamoyl phosphate synthase
ahpC	*llmg_0356*	2.91E-07	4.5	alkyl hydroperoxide reductase subunit C
cspD	*llmg_1256*	1.86E-06	4.5	cold shock-like protein
llmg_0333	*llmg_0333*	2.39E-06	4.4	tRNA synthetase
pyrP	*llmg_0891*	3.33E-07	4.3	pyrimidine metabolism
bglS	*llmg_0190*	1.23E-07	4.1	phospho-β-glucosidase
mvaA	*llmg_0931*	6.90E-07	4.0	hydroxymethylglutaryl-CoA reductase
plpD	*llmg_0340*	3.98E-07	4.0	D-methionine-binding lipoprotein precursor
glnA	*llmg_2484*	2.11E-06	3.9	glutamine synthetase
llmg_1920	*llmg_1920*	1.99E-05	3.8	HD superfamily hydrolase
busAA	*llmg_1048*	3.76E-07	3.8	glycine betaine/proline ABC transporter
hrcA	*llmg_1576*	2.40E-07	3.7	heat-inducible transcription repressor
llmg_0300	*llmg_0300*	4.39E-07	3.7	protein of unknown function
metE2	*llmg_1849*	1.38E-06	3.7	cysteine and methionine metabolism
llmg_1103	*llmg_1103*	3.59E-07	3.7	protein of unknown function
argE	*llmg_0536*	3.59E-05	3.7	arginine metabolism
pmi	*llmg_1789*	1.33E-06	3.7	mannose-6-phosphate isomerase
llmg_0877	*llmg_0877*	5.94E-05	3.6	proten of unknown function
llmg_1806	*llmg_1806*	5.20E-07	3.6	protein of unknown function
llmg_0872	*llmg_0872*	2.54E-07	3.6	protein of unknown function
rplM	*llmg_2546*	3.53E-06	3.6	ribosomal protein
rpsA	*llmg_1724*	2.45E-05	3.6	ribosomal protein
llmg_1811	*llmg_1811*	2.35E-07	3.5	tRNA (guanine-N(7))-methyltransferase
gnd	llmg_0586	1.18E-06	3.5	6-phosphogluconate dehydrogenase

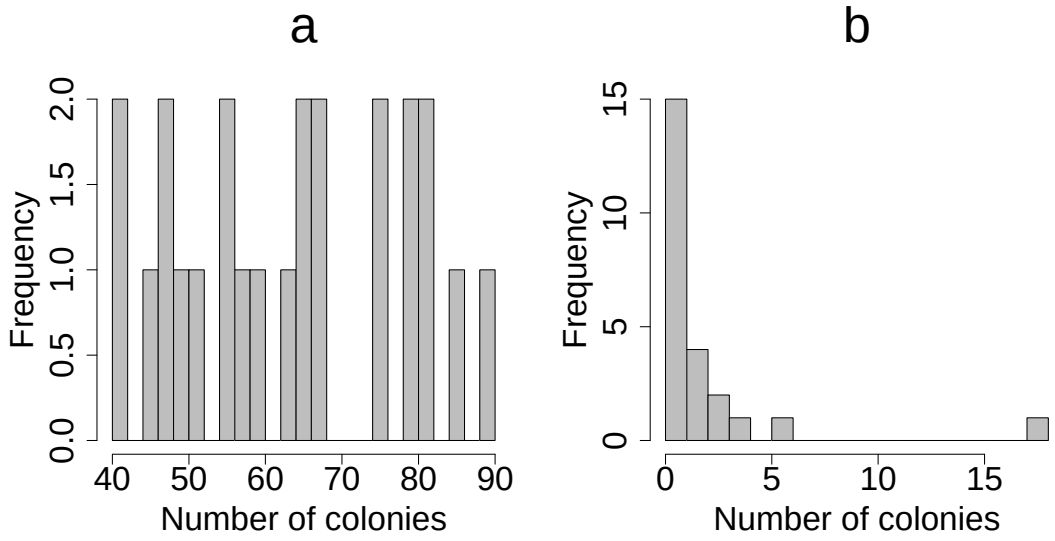
dnaI	*llmg_1808*	7.12E-07	3.5	primosomal protein DnaI
llmg_0508	*llmg_0508*	9.98E-07	3.5	cysteine synthase
rplS	*llmg_1671*	0.000160381	3.4	ribosomal protein
llmg_1762	*llmg_1762*	5.19E-06	3.4	protein of unknown function
pepT	*llmg_1994*	3.21E-06	3.3	tripeptide aminopeptidase
llmg_0417	*llmg_0417*	1.81E-06	3.3	protein of unknown function
llmg_0097	*llmg_0097*	1.91E-06	3.3	putative flavoprotein oxygenase
noxB	*llmg_1734*	2.07E-06	3.3	NADH dehydrogenase
llmg_1584	*llmg_1584*	8.51E-07	3.3	phosphatase
enoB	*llmg_pseudo08*	1.72E-06	3.3	pseudogene 08 (enolase)
llmg_1807	*llmg_1807*	1.26E-06	3.3	nitroreductase family protein
rplM	*llmg_2546*	9.53E-06	3.2	ribonuclease HIII
guaB	*llmg_0230*	2.68E-06	3.2	inositol-5-monophosphate dehydrogenase
llmg_0095	*llmg_0095*	2.20E-06	3.1	putative esterase
dnaB	*llmg_1809*	3.42E-06	3.1	chromosome replication initiation/membrane attachment protein
llmg_1089	*llmg_1089*	9.11E-06	3.1	protein of unknown function
fruC	*llmg_1569*	5.51E-05	3.0	1-phosphofructokinase
pepC	*llmg_2069*	1.02E-06	3.0	hydrolase
pyrF	*llmg_1107*	1.31E-06	3.0	pyrimidine metabolism
pepN	*llmg_0319*	2.87E-06	3.0	pepdidase N
llmg_0873	*llmg_0873*	1.78E-06	3.0	protein of unknown function
thiD1	*llmg_1217*	2.53E-05	2.9	phosphomethylpyrimidine kinase
llmg_1127	*llmg_1127*	5.63E-06	2.9	protein of unknown function
glnR	*llmg_2485*	0.00016258	2.9	glutamine synthetase repressor
busAB	*llmg_1049*	1.53E-05	2.9	glycine betaine/proline ABC transporter
llmg_1550	*llmg_1550*	3.96E-06	2.9	GroEl-homologous protein
llmg_0506	*llmg_0506*	2.64E-06	2.8	cell wall-associated protein
gerCA	*llmg_1111*	4.18E-06	2.8	heptaprenyl diphosphate synthase component I
cmhR	*llmg_0947*	3.82E-06	2.8	transcriptional regulator
noxA	*llmg_1735*	1.26E-06	2.8	NADH dehydrogenase
fruA	*llmg_1568*	3.34E-06	2.8	PTS system, fructose specific IIBC components
fruR	*llmg_1570*	1.68E-05	2.8	lactose transport regulator, fructose operon transcriptional repressor
nadR	*llmg_2241*	5.76E-06	2.8	putative nicotinamide-nucleotide adenylyltransferase
llmg_0781	*llmg_0781*	0.000189108	2.7	protein of unknown function
vicX	*llmg_0412*	2.02E-06	2.7	ribonuclease Z
llmg_0704	*llmg_0704*	5.69E-06	2.7	protein of unknown function
thrC	*llmg_2387*	4.19E-06	2.7	threonine synthase
menE	*llmg_1832*	3.38E-06	2.7	O-succinylbenzoic acid-CoA ligase
aldC	*llmg_1464*	3.02E-06	2.7	acetolactate decarboxylase, butanoate metabolism
rpsF	*llmg_2475*	0.000128226	2.6	ribosomal protein
oppB2	*llmg_2026*	7.03E-05	2.6	peptide ABC transporter
menA	*llmg_0197*	2.56E-05	2.6	1,4-dihydroxy-2-naphthoate octaprenyltransferase
llmg_0685	*llmg_0685*	8.28E-05	2.6	protein of unknown function
llmg_2386	*llmg_2386*	6.76E-06	2.6	putative MATE family transporter
llmg_2423	*llmg_2423*	8.10E-06	2.6	protein of unknown function

pyrR	*llmg_0890*	1.92E-05	2.6	pyrimidine metabolism
dar	*llmg_0339*	6.55E-06	2.6	acetoin(diacetyl)reductase
rpmE	*llmg_0906*	5.08E-06	2.6	ribosomal protein
rpsD	*llmg_0296*	0.000121058	2.6	ribosomal protein
rpsL	*llmg_2558*	6.96E-06	2.6	ribosomal protein
llmg_0007	*llmg_0007*	2.24E-05	2.6	protein of unknown function
thiL	*llmg_0930*	5.36E-06	2.6	acetyl-CoA C-acetyltransferase
rex	*llmg_1514*	6.13E-06	2.5	redox-sensing transcriptional repressor Rex
llmg_0241	*llmg_0241*	2.68E-05	2.5	protein of unknown function
llmg_0538	*llmg_0538*	0.000248717	2.5	protein of unknown function
pgk	*llmg_0253*	5.51E-05	2.5	phosphoglycerate kinase
mntH	*llmg_1490*	3.62E-06	2.5	putative proton-dependent manganese transporter
ispB	*llmg_1110*	4.46E-06	2.5	heptaprenyl diphosphate synthase component II
kinD	*llmg_1649*	1.20E-05	2.5	CesS sensor kinase
frdC	*llmg_1441*	6.78E-06	2.5	fumarate reductase flavoprotein subunit
arcB	*llmg_2312*	9.00E-10	-92.9	ornithine carbamoyltransferase
arcD1	*llmg_2311*	1.33E-06	-48.7	arginine/ornithine antiporter
arcA	*llmg_2313*	6.53E-09	-48.7	arginine deiminase
arcC1	*llmg_2310*	2.53E-06	-44.9	carbamate kinase
arcC2	*llmg_2309*	4.85E-06	-39.5	carbamate kinase
llmg_0959	*llmg_0959*	1.06E-07	-31.8	β-glucosidase
pgmB	*llmg_0456*	9.94E-07	-26.9	β-phosphoglucomutase
llmg_0960	*llmg_0960*	9.22E-07	-23.4	β-glucosidase
yfiA	*llmg_0616*	7.14E-08	-18.6	putative sigma 54 modulation protein
trePP	*llmg_0455*	2.53E-05	-16.9	putative trehalose/maltose hydrolase
rpe2	*llmg_0957*	1.67E-07	-16.1	ribulose phosphate 3-epimerase
mtlR	*llmg_0023*	5.64E-09	-12.8	transcriptional regulator mtl mannitol operon MtlR
llmg_0454	*llmg_0454*	8.45E-06	-8.3	β-glucoside-specific PTS system IIABC component
als	*llmg_1309*	2.37E-08	-7.8	acetolactate synthase
TrePP	*llmg_0455*	0.000260121	-7.5	putative trehalose/maltose hydrolase
glpD	*llmg_1098*	1.28E-08	-7.3	glycerol 3-phosphate dehydrogenase
llmg_1990	*llmg_1990*	9.09E-05	-6.9	protein of unknown function
glpD	*llmg_1098*	1.15E-07	-6.8	glycerol 3-phosphate dehydrogenase
rpiB	*llmg_0958*	0.000159752	-6.1	ribose 5-phosphate isomerase B
arcT	*llmg_2308*	1.69E-08	-6.0	arginine deiminase pathway
llmg_2431	*llmg_2431*	2.16E-08	-5.8	protein of unknown function
llmg_1299	*llmg_1299*	5.47E-08	-5.3	protein of unknown function
llmg_1302	*llmg_1302*	9.10E-07	-5.3	putative membrane protein
adhA	*llmg_1991*	5.62E-07	-5.1	alcohol dehydrogenase
glpF2	*llmg_1097*	3.81E-07	-4.8	glycerol uptake facilitator
mtlF	*llmg_0024*	0.001312068	-4.8	PTS system, mannitol-specific IIA component
llmg_1300	*llmg_1300*	9.13E-06	-4.6	protein of unknown function
llmg_1385	*llmg_1385*	1.52E-07	-4.4	protein of unknown function
llmg_1301	*llmg_1301*	9.02E-07	-4.3	protein of unknown function
gntP	*llmg_2467*	3.69E-06	-4.1	gluconate:H^+ symporter
mtlA	*llmg_0022*	2.07E-07	-4.1	PTS system, mannitol-specific IIBC component

rpsN	*llmg_2370*	7.06E-06	-4.1	ribosomal protein
orf24	*llmg_1384*	3.18E-07	-3.9	protein of unknown function
rbsD	*llmg_0786*	4.09E-06	-3.9	ribosomal protein
rgpE	*llmg_0216*	2.76E-07	-3.8	glycosyltransferase
rgpF	*llmg_0217*	5.88E-07	-3.8	rhamnosyltransferase
rbsC	*llmg_0788*	5.33E-05	-3.8	ribosomal protein
llmg_1303	*llmg_1303*	1.10E-06	-3.8	tryptophan-rich sensory protein
llmg_1396	*llmg_1396*	1.20E-06	-3.8	protein of unknown function
ltrD	*llmg_1375*	2.28E-06	-3.8	LtrD protein
ltrC	*llmg_1376*	1.96E-06	-3.8	putative DNA primase
glgD	*llmg_1873*	6.08E-07	-3.7	protein of unknown function
llmg_1468	*llmg_1468*	1.22E-06	-3.6	protein of unknown function
llmg_1497	*llmg_1497*	1.25E-06	-3.5	putative hydrolase
orf30	*llmg_1377*	1.48E-05	-3.5	protein of unknown function
matR	*llmg_1371*	5.34E-07	-3.5	maturase
clpB	*llmg_0986*	5.50E-07	-3.5	ATP-dependent Clp protease
ascB	*llmg_0751*	5.62E-05	-3.4	6-phospho-β-glucosidase
rplE	*llmg_2371*	1.74E-06	-3.4	ribosomal protein
llmg_0286	*llmg_0286*	5.86E-07	-3.4	protein of unknown function
phoU	*llmg_1895*	2.31E-06	-3.3	phosphate transport system regulator
orf28	*llmg_1379*	1.44E-06	-3.3	protein of unknown function
orf26	*llmg_1382*	3.47E-05	-3.2	protein of unknown function
chb	*llmg_2200*	5.51E-05	-3.2	putative chitin binding protein
rplX	*llmg_2372*	5.54E-06	-3.2	ribosomal protein
cstA	*llmg_0430*	7.43E-07	-3.2	carbon starvation protein A
llmg_0453	*llmg_0453*	4.53E-05	-3.1	PTS system, β-glucosides-specific IIA component
llmg_0963	*llmg_0963*	0.000315217	-3.1	PTS system, IIC component
llmg_2465	*llmg_2465*	1.45E-06	-3.1	protein of unknown function
llrA	*llmg_0908*	5.81E-06	-3.0	two-component system regulator llrA
llmg_0047	*llmg_0047*	2.71E-06	-3.0	protein of unknown function
llmg_1496	*llmg_1496*	2.12E-06	-3.0	protein of unknown function
mtlA	*llmg_0022*	1.58E-06	-3.0	PTS system, mannitol-specific IIBC component
llmg_0228	*llmg_0228*	1.83E-06	-3.0	protein of unknown function
llmg_0053	*llmg_0053*	1.70E-05	-2.9	protein of unknown function
rpsN	*llmg_2370*	0.000431286	-2.9	ribosomal protein
ptcA	*llmg_0438*	2.63E-06	-2.9	cellobiose-specific PTS IIA component
orf18	*llmg_1390*	2.26E-05	-2.9	protein of unknown function
orf22	*llmg_1386*	3.43E-05	-2.9	protein of unknown function
llmg_1993	*llmg_1993*	5.54E-05	-2.8	protein of unknown function
malG	*llmg_0737*	4.36E-05	-2.8	maltose ABC transporter permease
matR	*llmg_1371*	6.58E-06	-2.8	maturase
llmg_1517	*llmg_1517*	8.35E-06	-2.7	putative acidic phosphatase
recN	*llmg_1685*	1.07E-05	-2.7	DNA repair protein
cluA	*llmg_1398*	2.31E-05	-2.7	protein of unknown function
llmg_1093	*llmg_1093*	2.56E-05	-2.7	protein of unknown function
llmg_1467	*llmg_1467*	3.54E-05	-2.7	protein of unknown function

llmg_0510	*llmg_0510*	5.13E-06	-2.7	protein of unknown function
ponA	*llmg_0511*	1.06E-05	-2.7	penicillin-binding protein 1A
llmg_0005	*llmg_0005*	0.000645883	-2.7	protein of unknown function
rplN	*llmg_2373*	0.000259466	-2.7	ribosomal protein
chiC	*llmg_2199*	3.08E-06	-2.7	acidic endochitinase
llmg_pseudo77	*llmg_pseudo77*	5.57E-06	-2.7	pseudogene 77(hypothetical protein)
arcD2	*llmg_2307*	6.72E-05	-2.7	arginine deiminase pathway
cstA	*llmg_0430*	3.83E-05	-2.7	carbon starvation protein A
glnQ	*llmg_1943*	2.42E-05	-2.7	glutamine ABC transporter
llmg_2483	*llmg_2483*	7.11E-06	-2.7	protein of unknown function
gntK	*llmg_2468*	1.39E-05	-2.7	gluconate kinase, pentose phosphate pathway
llmg_1391	*llmg_1391*	9.30E-06	-2.6	protein of unknown function
orf18	*llmg_1390*	2.17E-05	-2.6	protein of unknown function
mapA	*llmg_0745*	4.65E-06	-2.6	maltose phosphorylase
ocd	*llmg_1149*	3.95E-05	-2.6	ornithine cyclodeaminase
rlx	*llmg_1372*	1.08E-05	-2.6	relaxase LtrB
rplB	*llmg_2380*	0.000163961	-2.5	ribosomal protein
llmg_1093	*llmg_1093*	1.81E-05	-2.5	protein of unknown function
snf	*llmg_2319*	5.47E-06	-2.5	helicase

S4. Significant expression changes of the genes during growth of MG1363 Lac$^+$ on lactose as compared to growth on undefined carbon sources of the rich M17 medium.



S5. Distribution of colonies on selective plates in a fluctuation assay. a. The number of MGLac+ colonies on CDM supplemented with lactose after plating 24 individual cultures. b. The number of colonies on CDM supplemented with rifampicin after plating 24 individual cultures. The number of cells plated per culture in panel a was $1.6x10^8$, while twice as many cells were plated for the cultures shown in panel b.

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